

# EXHIBIT 1

Amino acid sequence of insert of Plasmid M15pREP (pQE-Ct-Uni ) #37.

MRGSHHHHHHGSACELGTPGRRVPDPTKESLSNKISLTGDTNLTNCYLDNLRYILAIL  
QKTPNEGA AVTITDYL SFFDTQKEGIYFAKNLTPESGGAIGYASPN SPTVEIRD TIGPV  
IFENNTCCRPFTSSNPNA AVNKIREGGAIHAONLYINHNDVVGF MKNFSYVRGGAIST  
ANTFV VSENQSCFLFMDNICIQNTAGKGGAIYAGTSNSFESNNCDLFFINNACCAGGA  
IFSPICSLTGNRGNIVFYNNRCFKNVETASSEASDGGAIKVTTRLDVTGNRGRIFFSDN  
ITKNYGGAIYAPVVTLVDNGPTYFINNVANNKGGAIYIDGTSNSKISADRHAIIFNENI  
VTNVTSANGTSTSANPPRRNAITVASSSGEILLGAGSSQNLI FYDPIEVS NAGVSVSFN  
KEADQTG SVVFSGATVNSADFHQRNLQTKTPAPLTL SNGFLCIEDHAQLTVNRFTQTGG  
VVSLGNGAVLSCYKNGAGNSASNASITLKHIGLNLSSILKSGAEIPLLWVEPTNNSNNY  
TADTAATFSLSDVKLSLIDDYGN SPYESTDLTHALSSQPMLSISEASDNQLRSDDMDFS  
GLNVPHYGWQGLWSWGWA KTQDPEPASSATITDPKKANRFHRTL LLLTWLPAGYVPSPKH  
RSPLIANTLWGNMLLATESLKN SAELT PSDHPFWGITGGGLGMMVYQEPRENHPGFHMR  
SSGYFAGMIAGQTH TFS LKFSQTYTKLNERYAKNNVSSKNYSCQGEMLFSLQEGFLLAK  
LVGLYSYGDHNC HHFYTQGENLTSQGTFRSQTMGGAVFFDLPMKPF GSTHILTAPFLGA  
LGIYSSLSHFTEVGAYPRSFSTKTPLINVLVPIGVKGSFMNATQRPQAWTVELAYQPVL  
YRQELEIATQLLASKGIWFGSGSPSSRHMSYKISQQTQPLSWLTLHFQYHGFYSSSTF  
CNYLNGEIALRF.

Nucleic acid sequence of Plasmid M15pREP (pQE-Ct-Uni ) #37.

ATGAGAGGATCGCATCACCATCACCATCACGGATCCGCATGCGAGCTCGGTACCCCGGGTC  
GACGGGTTCCAGATCCTACGAAAGAGTCGCTATCAAATAAAATTAGTTTGACAGGAGACAC  
TCACAATCTCACTAACTGCTATCTCGATAACCTACGCTACATACTGGCTATTCTACAAAAA  
CTCCCAATGAAGGAGCTGCTGTCACAATAACAGATTACCTAAGCTTTTTTGATACACAAAA  
AGAAGGTATTTATTTTGCAAAAAATCTCACCCCTGAAAGTGGTGGTGCGATTGGTTATGCG  
AGTCCCAATTCTCCTACCGTGGAGATTCGTGATACAATAGGTCCTGTAATCTTTGAAAATAA  
TACTTGTTGCAGACCATTTACATCGAGTAATCCTAATGCAGCTGTTAATAAAATAAGAGAA  
GGCGGAGCCATTCATGCTCAAATCTTTACATAAATCACAATCATGATGTGGTTCGGATTTAT  
GAAGAACTTTTCTTATGTCCGAGGAGGAGCCATTAGTACCGCTAATACTTTGTTGTGAGCG  
AGAATCAGTCTTGTTTTCTCTTTATGGACAACATCTGTATTCAAATAACAGCAGGAAAA  
GGTGGCGCTATCTATGCTGGAACGAGCAATTCTTTGAGAGTAATAACTGCGATCTCTTCTT  
TATCAATAACGCCTGTTGTGCAGGAGGAGCGATCTTCTCCCTATCTGTTCTCTAACAGGAA  
ATCGTGGTAACATCGTTTTCTATAACAATCGCTGCTTTAAAAATGTAGAAACAGCTTCTTCA  
GAAGCTTCTGATGGAGGAGCAATTAAAGTAACTACTCGCCTAGATGTTACAGGCAATCGTG  
GTAGGATCTTTTTTAGTGACAATATCACAAAAATTATGGCGGAGCTATTTACGCTCCTGTA

GTTACCCTAGTGGATAATGGCCCTACCTACTTTATAAACAATGTCGCCAATAATAAGGGGG  
GCGCTATCTATATAGACGGAACCAGCAACTCCAAAATTTCTGCCGACCGCCATGCTATTATT  
TTTAATGAAAATATTGTGACTAATGTAAGTGTGCAAATGGTACCAGTACGTCAGCTAATC  
CTCCTAGAAGAAATGCAATAACAGTAGCAAGCTCCTCTGGTGAAATTCTATTAGGAGCAGG  
GAGTAGCCAAAATTTAATTTTTTATGATCCTATTGAAGTTAGCAATGCAGGGGTCTCTGTGT  
CCTTCAATAAGGAAGCTGATCAAACAGGCTCTGTAGTATTTTCAGGAGCTACTGTTAATTCT  
GCAGATTTTCATCAACGCAATTTACAAACAAAAACACCTGCACCCCTTACTCTCAGTAATG  
GTTTTCTATGTATCGAAGATCATGCTCAGCTTACAGTGAATCGATTACACAAAACCTGGGGGT  
GTTGTTTCTCTTGGGAATGGAGCAGTTCTGAGTTGCTATAAAAATGGTGCGAGGAAATTCTGC  
TAGCAATGCCTCTATAACACTGAAGCATATTGGATTGAATCTTTCTTCCATTCTGAAAAGTG  
GTGCTGAGATTCTTTTATTGTGGGTAGAGCCTACAAATAACAGCAATAACTATACAGCAGA  
TACTGCAGCTACCTTTTCATTAAGTGATGTAAAACCTCTCACTCATTGATGACTATGGGAATT  
CTCCTTATGAATCCACAGATCTAACCCATGCTCTGTCATCACAGCCTATGCTATCTATTTCT  
GAGGCTAGTGATAACCAGCTAAGATCTGATGATATGGATTTCTCGGGACTAAATGTCCCTC  
ATTATGGATGGCAAGGACTTTGGAGTTGGGGCTGGGCAAAAACCTCAAGATCCAGAACCAG  
CATCTTCAGCAACAATCACAGATCCCAAAAAAGCCAATAGATTCCATAGAACCTTATTACT  
GACTTGGCTTCCTGCTGGGTATGTTCTAGCCCGAAACACAGAAGTCCCCTCATAGCGAAT  
ACCTTATGGGGGAATATGCTGCTTGCAACAGAAAGCTTAAAAAATAGTGCAGAACTGACAC  
CTAGTGATCATCCTTTCTGGGGAATTACAGGAGGAGGACTAGGCATGATGGTTTACCAAGA  
ACCTCGAGAAAATCATCCTGGATTCCATATGCGCTCTTCCGGATACTTTGCGGGGATGATA  
GCAGGGCAAACACATACCTTCTCATTGAAATTCAGTCAGACCTACACCAAACCTCAATGAGC  
GTTACGCAAAAAACAACGTATCTTCTAAAAATTACTCATGCCAAGGAGAAATGCTCTTCTC  
ATTGCAAGAAGGTTTCTTGCTGGCTAAATTAGTTGGTCTTTACAGCTATGGAGATCATAACT  
GTCACCATTTCTATACCCAAGGAGAAAATCTAACATCTCAAGGGACGTTCCGTAGTCAAAC  
GATGGGAGGTGCTGTTTTTTTTGATCTCCCTATGAAACCCTTTGGATCAACGCATATACTGA  
CAGCTCCCTTTTTAGGTGCTCTTGGTATTTATTCTAGCCTGTCTCACTTTACTGAGGTGGGAG  
CCTATCCGCGAAGCTTTTCTACAAAGACTCCTTTGATCAATGTCCTAGTCCCTATTGGAGTT  
AAAGGTAGCTTTATGAATGCTACCCAAAGACCTCAAGCCTGGACTGTAGAATTGGCATACC  
AACCCGTTCTGTATAGACAAGAACTAGAGATCGCGACCCAGCTCCTAGCCAGTAAAGGTAT  
TTGGTTTGGTAGTGGAAGCCCCTCATCGCGTCATGCCATGTCCTATAAAATCTCACAGCAAA  
CACAACTTTGAGTTGGTTAACTCTCCATTTCCAGTATCATGGATTCTACTCCTCTTCAACCT  
TCTGTAATTATCTCAATGGGGAAATTGCTCTGCGATTCTAA



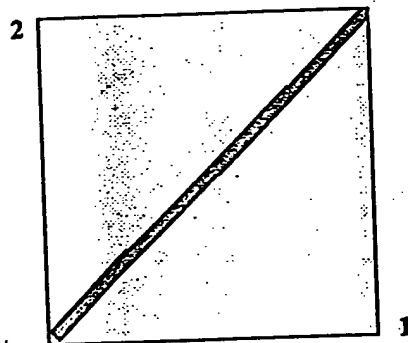
## Blast 2 Sequences results

BLAST 2 SEQUENCES RESULTS VERSION BLASTP 2.2.1 [Aug-1-2001]

Matrix: BLOSUM62 gap open: 11 gap extension: 1  
x\_dropoff: 50 expect: 10.0 wordsize: 3 Filter ☒ Align

Sequence 1 lc|seq\_1 Length 956 (1..956)

Sequence 2 lc|seq\_2 Length 965 (1..965)



NOT: (score and expect value) is calculated based on the size of nr database

Score = 1885 bits (4884), Expect = 0.0  
Identities = 925/934 (99%), Positives = 930/934 (99%)

Query: 23 VPDPTKESLSNKKISLTGDTNLTNCYLDNLRILAILQKTPNEGAAVTITDYLSTFDQK 82  
VPDPTKESLSNKKISLTGDTNLTNCYLDNLRILAILQKTPNEGAAVTITDYLSTFDQK  
Sbjct: 32 VPDPTKESLSNKKISLTGDTNLTNCYLDNLRILAILQKTPNEGAAVTITDYLSTFDQK 91

Query: 83 EGIYFAKNLTPESGGAIGYASPNSTVEIRDITGPVIFENNTCCRPFTSSNPNAAVNKIR 142  
EGIYFAKNLTPESGGAIGYASPNSTVEIRDITGPVIFENNTCCRPFTSSNPNAAVNKIR  
Sbjct: 92 EGIYFAKNLTPESGGAIGYASPNSTVEIRDITGPVIFENNTCCRPFTSSNPNAAVNKIR 151

Query: 143 EGGAIHAQNLYINHNDVVGFMKNFSYVRGGAISTANTFVVSSENQSCFLFMDNICIQTNT 202  
EGGAIHAQNLYINHNDVVGFMKNFSYVRGGAISTANTFVVSSENQSCFLFMDNICIQTNT  
Sbjct: 152 EGGAIHAQNLYINHNDVVGFMKNFSYVRGGAISTANTFVVSSENQSCFLFMDNICIQTNT 211

Query: 203 AGKGGAIYAGTSNSFESNNCDLFFINNACCAGGAIFSPICSLTGNRGNIVFYNNRCFKNV 262  
AGKGGAIYAGTSNSFESNNCDLFFINNACCAGGAIFSPICSLTGNRGNIVFYNNRCFKNV  
Sbjct: 212 AGKGGAIYAGTSNSFESNNCDLFFINNACCAGGAIFSPICSLTGNRGNIVFYNNRCFKNV 271

Query: 263 ETASSEASDGGAIKVTTRLDVTGNRGRIFSDNITKNYGGAIYAPVVTLDNGPTYFINN 322  
ETASSEASDGGAIKVTTRLDVTGNRGRIFSDNITKNYGGAIYAPVVTLDNGPTYFINN  
Sbjct: 272 ETASSEASDGGAIKVTTRLDVTGNRGRIFSDNITKNYGGAIYAPVVTLDNGPTYFINN 331

Query: 323 VANKGGAIYIDGTSNSKISADRHAIIFNENIVTNVTSANGTSTSANPPRRNAITVASSS 382  
+ANKGGAIYIDGTSNSKISADRHAIIFNENIVTNVT+ANGTSTSANPPRRNAITVASSS  
Sbjct: 332 IANKGGAIYIDGTSNSKISADRHAIIFNENIVTNVTNANGTSTSANPPRRNAITVASSS 391

Query: 383 GEILLGAGSSQNLIFYDPIEVSNAGVSVSFNKEADQTGSVVFSGATVNSADFHQRNLQTK 442  
GEILLGAGSSQNLIFYDPIEVSNAGVSVSFNKEADQTGSVVFSGATVNSADFHQRNLQTK  
Sbjct: 392 GEILLGAGSSQNLIFYDPIEVSNAGVSVSFNKEADQTGSVVFSGATVNSADFHQRNLQTK 451

Query: 443 TPAPLTLNGLFCIEDHAQLTVNRFTQTGGVSLGNGAVLSCYKNGAGNSASNASITLKH 502  
TPAPLTLNGLFCIEDHAQLTVNRFTQTGGVSLGNGAVLSCYKNGAGNSASNASITLKH  
Sbjct: 452 TPAPLTLNGLFCIEDHAQLTVNRFTQTGGVSLGNGAVLSCYKNGAGNSASNASITLKH 511

Query: 503 IGLNLSSILKSGAEIPLLWVEPTNNSNNTADTAATFSLSDVKLSLIDYGNSPYESTDL 562  
IGLNLSSILKSGAEIPLLWVEPTNNSNNTADTAATFSLSDVKLSLIDYGNSPYESTDL

Friday, September 6, 2001

Blast Result

Subject: 512 IGLNLSSILKSGAEIPLLWVEPTNNSNNYTADTAATFSLSDVKLSLIDYGNSPYESTDL 571  
 Query: 563 THALSSQPMLSISEASDNQLRSDDMDFSGLVNPHYGWQGLWSGWAKTQDPEPASSATIT 622  
 THALSSQPMLSISEASDNQLRSDDMDFSGLVNPHYGWQGLW+GWAKTQDPEPASSATIT  
 Subject: 572 THALSSQPMLSISEASDNQLRSDDMDFSGLVNPHYGWQGLWTGWAKTQDPEPASSATIT 631  
 Query: 623 DPKKANRFHRTLLLTWLPAGYVPSPKHRSPLIANTLWGNMMLLATESLKNSAELTPSDHPP 682  
 DP+KANRFHRTLLLTWLPAGYVPSPKHRSPLIANTLWGNMMLLATESLKNSAELTPSDHPP  
 Subject: 632 DPKKANRFHRTLLLTWLPAGYVPSPKHRSPLIANTLWGNMMLLATESLKNSAELTPSDHPP 691  
 Query: 683 WGITGGGLGMMVYQEPRENHPGFHMRRSSGYFAGMIAGQTHTFSLKFSQTYTKLNERYAKN 742  
 WGITGGGLGMMVYQ+PRENHPGFHMRRSSGY AGMIAGQTHTFSLKFSQTYTKLNERYAKN  
 Subject: 692 WGITGGGLGMMVYQDPRENHPGFHMRRSSGYSAGMIAGQTHTFSLKFSQTYTKLNERYAKN 751  
 Query: 743 NVSSKNYSCQGEMLFSLQEGFLLAKLVGLYSYGDHNCCHFYTQGENLTSQGTFRSQTMGG 802  
 NVSSKNYSCQGEMLFSLQEGFLL KLVGLYSYGDHNCCHFYTQGENLTSQGTFRSQTMGG  
 Subject: 752 NVSSKNYSCQGEMLFSLQEGFLLTKLVGLYSYGDHNCCHFYTQGENLTSQGTFRSQTMGG 811  
 Query: 803 AVFFDLPMKPFPGSTHILTAPFLGALGIYSSLSHFTEVGAYPRSFSTKTPLINVLVPIGVK 862  
 AVFFDLPMKPFPGSTHILTAPFLGALGIYSSLSHFTEVGAYPRSFSTKTPLINVLVPIGVK  
 Subject: 812 AVFFDLPMKPFPGSTHILTAPFLGALGIYSSLSHFTEVGAYPRSFSTKTPLINVLVPIGVK 871  
 Query: 863 GSFMNATQRPQAWTVELAYQPVLRYRQELEIATQLLASKGIWFGSGSPSSRHAMSYSKISQQ 922  
 GSFMNATQRPQAWTVELAYQPVLRYRQE IATQLLASKGIWFGSGSPSSRHAMSYSKISQQ  
 Subject: 872 GSFMNATQRPQAWTVELAYQPVLRYRQEPGIATQLLASKGIWFGSGSPSSRHAMSYSKISQQ 931  
 Query: 923 TQPLSWLTLHFQYHGFYSSSTFCNYLNGEIALRF 956  
 TQPLSWLTLHFQYHGFYSSSTFCNYLNGEIALRF  
 Subject: 932 TQPLSWLTLHFQYHGFYSSSTFCNYLNGEIALRF 965

CPU time: 0.36 user secs. 0.02 sys. secs 0.38 total secs.

Gapped  
 Lambda K H  
 0.316 0.132 0.396

Gapped  
 Lambda K H  
 0.267 0.0410 0.140

Matrix: BLOSUM62

Gap Penalties: Existence: 11, Extension: 1

Number of Hits to DB: 12,524

Number of Sequences: 0

Number of extensions: 873

Number of successful extensions: 15

Number of sequences better than 10.0: 1

Number of HSP's better than 10.0 without gapping: 1

Number of HSP's successfully gapped in prelim test: 0

Number of HSP's that attempted gapping in prelim test: 0

Number of HSP's gapped (non-prelim): 1

length of query: 956

length of database: 239,316,239

effective HSP length: 131

effective length of query: 825

effective length of database: 206,523,009

effective search space: 170381482425

effective search space used: 170381482425

T: 9

A: 40

X1: 16 ( 7.3 bits)

X2: 129 (49.7 bits)

X3: 129 (49.7 bits)

S1: 41 (21.6 bits)

S2: 77 (34.3 bits)